W078

Exploring Predicted Musa Genes Using the GreenPhyl Comparative Genomics Database

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Room: Pacific Salon 6-7 (2nd Floor)
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With the increasing number of plant genomes being sequenced, a major challenge is to accurately transfer annotation from well characterized genomes to newly obtained sequences. GreenPhylDB is a database designed for comparative and functional genomics based on complete genome-derived gene sequences (Conte et al, 2008, Rouard M, Guignon V et al, 2011). The database currently includes gene sequences from 22 plant species, including Musa (representative of bananas and plantains). Genes from all these species are organized in clusters based on sequence similarity. The clusters (or families) are manually annotated (i.e. properly named and classified) and sequences included in each cluster are characterized by phylogenetic analysis in order to elucidate evolutionary relationships (e.g. orthologs, super-orthologs, in/out-paralogs) among genes. GreenPhyl provides a reliable (Martinez, 2011) and stable catalog of gene families useful for annotation on new genome sequences in plants. GreenPhyl has been particularly useful for studying the transcription factors of the Musa acuminata (Doubled Haploid Pahang) genome sequence recently published (D'hont et al, 2012). With its improved user interface, the new release of GreenPhyl (available at http://www.greenphyl.org) keeps the previous gene clustering quality and introduces additional features such as specific search engines (quick search, deep search, InterPro domain combination and GO family browser). This talk will present the latest development of the GreenPhyl version 3 and will give a few examples of gene family analyses in Musa.